

SEQUENCE LISTING

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<120> MODIFIED PHYTASES

<130> Modified Phytases

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<150> EP 97810175.6

<151> 1997-03-25

<160> 82

<170> PatentIn Ver. 2.1

<210> 1

<211> 444

<212> PRT

<213> Aspergillus niger

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35 40 45

Arg Val Thr Phe Ala Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro
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Thr Asp Ser Lys Gly Lys Lys Tyr Ser Ala Leu Ile Glu Glu Ile Gln
65 70 75 80

Gln Asn Ala Thr Thr Phe Asp Gly Lys Tyr Ala Phe Leu Lys Thr Tyr
85 90 95

Asn Tyr Ser Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Glu

10062843-020102

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Arg Asn Ile Val Pro Phe Ile Arg Ser Ser Gly Ser Ser Arg Val Ile		
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Ala Ser Gly Lys Lys Phe Ile Glu Gly Phe Gln Ser Thr Lys Leu Lys		
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Asp Pro Arg Ala Gln Pro Gly Gln Ser Ser Pro Lys Ile Asp Val Val		
165	170	175
Ile Ser Glu Ala Ser Ser Ser Asn Asn Thr Leu Asp Pro Gly Thr Cys		
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Thr Val Phe Glu Asp Ser Glu Leu Ala Asp Thr Val Glu Ala Asn Phe		
195	200	205
Thr Ala Thr Phe Val Pro Ser Ile Arg Gln Arg Leu Glu Asn Asp Leu		
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Ser Gly Val Thr Leu Thr Asp Thr Glu Val Thr Tyr Leu Met Asp Met		
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Cys Ser Phe Asp Thr Ile Ser Thr Ser Thr Val Asp Thr Lys Leu Ser		
245	250	255
Pro Phe Cys Asp Leu Phe Thr His Asp Glu Trp Ile Asn Tyr Asp Tyr		
260	265	270
Leu Gln Ser Leu Lys Lys Tyr Tyr Gly His Gly Ala Gly Asn Pro Leu		
275	280	285
Gly Pro Thr Gln Gly Val Gly Tyr Ala Asn Glu Leu Ile Ala Arg Leu		
290	295	300
Thr His Ser Pro Val His Asp Asp Thr Ser Ser Asn His Thr Leu Asp		
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Ser Ser Pro Ala Thr Phe Pro Leu Asn Ser Thr Leu Tyr Ala Asp Phe		
325	330	335
Ser His Asp Asn Gly Ile Ile Ser Ile Leu Phe Ala Leu Gly Leu Tyr		
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Asn Gly Thr Lys Pro Leu Ser Thr Thr Thr Val Glu Asn Ile Thr Gln		

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360

365

Thr Asp Gly Phe Ser Ser Ala Trp Thr Val Pro Phe Ala Ser Arg Leu
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Tyr Val Glu Met Met Gln Cys Gln Ala Glu Gln Glu Pro Leu Val Arg
385 390 395 400

Val Leu Val Asn Asp Arg Val Val Pro Leu His Gly Cys Pro Val Asp
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<211> 438

<212> PRT

<213> Aspergillus terreus

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Ser Pro Phe Pro Leu Asp Val Pro Asp Asp Cys His Ile Thr Phe Val
35 40 45

Gln Val Leu Ala Arg His Gly Ala Arg Ser Pro Thr Asp Ser Lys Thr
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Lys Ala Tyr Ala Ala Thr Ile Ala Ala Ile Gln Lys Asn Ala Thr Ala
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Leu Pro Gly Lys Tyr Ala Phe Leu Lys Ser Tyr Asn Tyr Ser Met Gly
85 90 95

Ser Glu Asn Leu Thr Pro Phe Gly Arg Asn Gln Leu Gln Asp Leu Gly
100 105 110

Ala Gln Phe Tyr Arg Arg Tyr Asp Thr Leu Thr Arg His Ile Asn Pro
115 120 125

Phe Val Arg Ala Ala Asp Ser Ser Arg Val His Glu Ser Ala Glu Lys
 130 135 140

Phe Val Glu Gly Phe Gln Asn Ala Arg Gln Gly Asp Pro His Ala Asn
 145 150 155 160

Pro His Gln Pro Ser Pro Arg Val Asp Val Val Ile Pro Glu Gly Thr
 165 170 175

Ala Tyr Asn Asn Thr Leu Glu His Ser Ile Cys Thr Ala Phe Glu Ala
 180 185 190

Ser Thr Val Gly Asp Ala Ala Ala Asp Asn Phe Thr Ala Val Phe Ala
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Pro Ala Ile Ala Lys Arg Leu Glu Ala Asp Leu Pro Gly Val Gln Leu
 210 215 220

Ser Ala Asp Asp Val Val Asn Leu Met Ala Met Cys Pro Phe Glu Thr
 225 230 235 240

Val Ser Leu Thr Asp Asp Ala His Thr Leu Ser Pro Phe Cys Asp Leu
 245 250 255

Phe Thr Ala Ala Glu Trp Thr Gln Tyr Asn Tyr Leu Leu Ser Leu Asp
 260 265 270

Lys Tyr Tyr Gly Tyr Gly Gly Gly Asn Pro Leu Gly Pro Val Gln Gly
 275 280 285

Val Gly Trp Ala Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val
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His Asp His Thr Cys Val Asn Asn Thr Leu Asp Ala Asn Pro Ala Thr
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Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Ser Asn
 325 330 335

Leu Val Ser Ile Phe Trp Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro
 340 345 350

Leu Ser Gln Thr Thr Val Glu Asp Ile Thr Arg Thr Asp Gly Tyr Ala
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Gln Cys Arg Ala Glu Lys Gln Pro Leu Val Arg Val Leu Val Asn Asp
 385 390 395 400

Arg Val Met Pro Leu His Gly Cys Ala Val Asp Asn Leu Gly Arg Cys
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<213> Aspergillus fumigatus

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 50 55 60

Ser Lys Lys Tyr Lys Lys Leu Val Thr Ala Ile Gln Ala Asn Ala Thr
 65 70 75 80

Asp Phe Lys Gly Lys Phe Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu
 85 90 95

Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Gln Leu Val Asn Ser
 100 105 110

Gly Ile Lys Phe Tyr Gln Arg Tyr Lys Ala Leu Ala Arg Ser Val Val
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Pro Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Ile Ala Ser Gly Glu
 130 135 140

Lys Phe Ile Glu Gly Phe Gln Gln Ala Lys Leu Ala Asp Pro Gly Ala
 145 150 155 160

Thr Asn Arg Ala Ala Pro Ala Ile Ser Val Ile Ile Pro Glu Ser Glu
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Thr Phe Asn Asn Thr Leu Asp His Gly Val Cys Thr Lys Phe Glu Ala
 180 185 190

Ser Gln Leu Gly Asp Glu Val Ala Ala Asn Phe Thr Ala Leu Phe Ala
 195 200 205

Pro Asp Ile Arg Ala Arg Ala Glu Lys His Leu Pro Gly Val Thr Leu
 210 215 220

Thr Asp Glu Asp Val Val Ser Leu Met Asp Met Cys Ser Phe Asp Thr
 225 230 235 240

Val Ala Arg Thr Ser Asp Ala Ser Gln Leu Ser Pro Phe Cys Gln Leu
 245 250 255

Phe Thr His Asn Glu Trp Lys Lys Tyr Asn Tyr Leu Gln Ser Leu Gly
 260 265 270

Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly
 275 280 285

Ile Gly Phe Thr Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val
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Gln Asp His Thr Ser Thr Asn Ser Thr Leu Val Ser Asn Pro Ala Thr
 305 310 315 320

Phe Pro Leu Asn Ala Thr Met Tyr Val Asp Phe Ser His Asp Asn Ser
 325 330 335

Met Val Ser Ile Phe Phe Ala Leu Gly Leu Tyr Asn Gly Thr Glu Pro
 340 345 350

Leu Ser Arg Thr Ser Val Glu Ser Ala Lys Glu Leu Asp Gly Tyr Ser
 355 360 365

Ala Ser Trp Val Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Thr Met
 370 375 380

Gln Cys Lys Ser Glu Lys Glu Pro Leu Val Arg Ala Leu Ile Asn Asp
 385 390 395 400

Arg Val Val Pro Leu His Gly Cys Asp Val Asp Lys Leu Gly Arg Cys
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Asn Trp Gly Glu Cys Phe Ser
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gct ctt tcg ctt tat tac ttg cta tcg agg tgagatctct acaatatctg 225
 Ala Leu Ser Leu Tyr Tyr Leu Leu Ser Arg
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 Val Ser Ala Gln Ala Pro Val
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gtc cag aat cat tca tgc aat acg gcg gac ggt gga tat caa tgc ttc 328
 Val Gln Asn His Ser Cys Asn Thr Ala Asp Gly Gly Tyr Gln Cys Phe
 25 30 35

ccc aat gtc tct cat gtt tgg ggt cag tac tcg ccg tac ttc tcc atc 376
 Pro Asn Val Ser His Val Trp Gly Gln Tyr Ser Pro Tyr Phe Ser Ile
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 Glu Gln Glu Ser Ala Ile Ser Glu Asp Val Pro His Gly Cys Glu Val

60

65

70

acc ttt gtg cag gtg ctc tcg cgg cat ggg gct agg tat ccg aca gag 472
 Thr Phe Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Glu
 75 80 85

tcg aag agt aag gcg tac tcg ggg ttg att gaa gca atc cag aag aat 520
 Ser Lys Ser Lys Ala Tyr Ser Gly Leu Ile Glu Ala Ile Gln Lys Asn
 90 95 100

gct acc tct ttt tgg gga cag tat gct ttt ctg gag agt tat aac tat 568
 Ala Thr Ser Phe Trp Gly Gln Tyr Ala Phe Leu Glu Ser Tyr Asn Tyr
 105 110 115

acc ctc ggc gcg gat gac ttg act atc ttc ggc gag aac cag atg gtt 616
 Thr Leu Gly Ala Asp Asp Leu Thr Ile Phe Gly Glu Asn Gln Met Val
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 Asp Ser Gly Ala Lys Phe Tyr Arg Arg Tyr Lys Asn Leu Ala Arg Lys
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aat act cct ttt atc cgt gca tca ggg tct gac cgt gtc gtt gcg tct 712
 Asn Thr Pro Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Val Ala Ser
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 Ala Glu Lys Phe Ile Asn Gly Phe Arg Lys Ala Gln Leu His Asp His
 170 175 180

ggc tcc aaa cgt gct acg cca gtt gtc aat gtg att atc cct gaa atc 808
 Gly Ser Lys Arg Ala Thr Pro Val Val Asn Val Ile Ile Pro Glu Ile
 185 190 195

gat ggg ttt aac aac acc ctg gac cat agc acg tgc gta tct ttt gag 856
 Asp Gly Phe Asn Asn Thr Leu Asp His Ser Thr Cys Val Ser Phe Glu
 200 205 210 215

aat gat gag cgg gcg gat gaa att gaa gcc aat ttc acg gca att atg 904
 Asn Asp Glu Arg Ala Asp Glu Ile Glu Ala Asn Phe Thr Ala Ile Met
 220 225 230

gga cct ccg atc cgc aaa cgt ctg gaa aat gac ctc cct ggc atc aaa 952
 Gly Pro Pro Ile Arg Lys Arg Leu Glu Asn Asp Leu Pro Gly Ile Lys
 235 240 245

ctt aca aac gag aat gta ata tat ttg atg gat atg tgc tct ttc gac 1000
 Leu Thr Asn Glu Asn Val Ile Tyr Leu Met Asp Met Cys Ser Phe Asp

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Thr Met Ala Arg Thr Ala His Gly Thr Glu Leu Ser Pro Phe Cys Ala			
265	270	275	
atc ttc act gaa aag gag tgg ctg cag tac gac tac ctt caa tct cta			1096
Ile Phe Thr Glu Lys Glu Trp Leu Gln Tyr Asp Tyr Leu Gln Ser Leu			
280	285	290	295
tca aag tac tac ggc tac ggt gcc gga agc ccc ctt ggc cca gct cag			1144
Ser Lys Tyr Tyr Gly Tyr Gly Ala Gly Ser Pro Leu Gly Pro Ala Gln			
300	305	310	
gga att ggc ttc acc aac gag ctg att gcc cga cta acg caa tcg ccc			1192
Gly Ile Gly Phe Thr Asn Glu Leu Ile Ala Arg Leu Thr Gln Ser Pro			
315	320	325	
gtc cag gac aac aca agc acc aac cac act cta gac tcg aac cca gcc			1240
Val Gln Asp Asn Thr Ser Thr Asn His Thr Leu Asp Ser Asn Pro Ala			
330	335	340	
aca ttt ccg ctc gac agg aag ctc tac gcc gac ttc tcc cac gac aat			1288
Thr Phe Pro Leu Asp Arg Lys Leu Tyr Ala Asp Phe Ser His Asp Asn			
345	350	355	
agc atg ata tcg ata ttc ttc gcc atg ggt ctg tac aac ggc acc cag			1336
Ser Met Ile Ser Ile Phe Phe Ala Met Gly Leu Tyr Asn Gly Thr Gln			
360	365	370	375
ccg ctg tca atg gat tcc gtg gag tcg atc cag gag atg gac ggt tac			1384
Pro Leu Ser Met Asp Ser Val Glu Ser Ile Gln Glu Met Asp Gly Tyr			
380	385	390	
gcg gcg tct tgg act gtt ccg ttt ggt gcg agg gct tac ttt gag ctc			1432
Ala Ala Ser Trp Thr Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Leu			
395	400	405	
atg cag tgc gag aag aag gag ccg ctt gtg cgg gta tta gtg aat gat			1480
Met Gln Cys Glu Lys Lys Glu Pro Leu Val Arg Val Leu Val Asn Asp			
410	415	420	
cgc gtt gtt cct ctt cat ggc tgc gca gtt gac aag ttt gga cgg tgc			1528
Arg Val Val Pro Leu His Gly Cys Ala Val Asp Lys Phe Gly Arg Cys			
425	430	435	
act ttg gac gat tgg gta gag ggc ttg aat ttt gca agg agc ggc ggg			1576
Thr Leu Asp Asp Trp Val Glu Gly Leu Asn Phe Ala Arg Ser Gly Gly			

440

445

450

455

aac tgg aag act tgt ttt acc cta taaagggcgt ttgctcattc ataagtgttg 1630
 Asn Trp Lys Thr Cys Phe Thr Leu

460

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gatttggttg ttctcaaggc cttctagcat atcgtcaagt gggataaatc acctatcctc 1750

catgtgtagg tgaaccgct cttgcatcaa cctcttggtt ttcagagtag tttcaccaaa 1810

catatcctcg tgtctctct tctgctcttc ggtctcatat tacactgttc tctatctata 1870

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1931

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<213> *Aspergillus nidulans*

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<211> 447

<212> PRT

<213> *Aspergillus nidulans*

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 20 25 30

Tyr Ser Pro Tyr Phe Ser Ile Glu Gln Glu Ser Ala Ile Ser Glu Asp
 35 40 45

Val Pro His Gly Cys Glu Val Thr Phe Val Gln Val Leu Ser Arg His
 50 55 60

Gly Ala Arg Tyr Pro Thr Glu Ser Lys Ser Lys Ala Tyr Ser Gly Leu
 65 70 75 80

Ile Glu Ala Ile Gln Lys Asn Ala Thr Ser Phe Trp Gly Gln Tyr Ala
 85 90 95

Phe Leu Glu Ser Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu Thr Ile

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Tyr Lys Asn Leu Ala Arg Lys Asn Thr Pro Phe Ile Arg Ala Ser Gly		
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Ser Asp Arg Val Val Ala Ser Ala Glu Lys Phe Ile Asn Gly Phe Arg		
145	150	155
Lys Ala Gln Leu His Asp His Gly Ser Lys Arg Ala Thr Pro Val Val		160
165	170	175
Asn Val Ile Ile Pro Glu Ile Asp Gly Phe Asn Asn Thr Leu Asp His		
180	185	190
Ser Thr Cys Val Ser Phe Glu Asn Asp Glu Arg Ala Asp Glu Ile Glu		
195	200	205
Ala Asn Phe Thr Ala Ile Met Gly Pro Pro Ile Arg Lys Arg Leu Glu		
210	215	220
Asn Asp Leu Pro Gly Ile Lys Leu Thr Asn Glu Asn Val Ile Tyr Leu		
225	230	235
Met Asp Met Cys Ser Phe Asp Thr Met Ala Arg Thr Ala His Gly Thr		240
245	250	255
Glu Leu Ser Pro Phe Cys Ala Ile Phe Thr Glu Lys Glu Trp Leu Gln		
260	265	270
Tyr Asp Tyr Leu Gln Ser Leu Ser Lys Tyr Tyr Gly Tyr Gly Ala Gly		
275	280	285
Ser Pro Leu Gly Pro Ala Gln Gly Ile Gly Phe Thr Asn Glu Leu Ile		
290	295	300
Ala Arg Leu Thr Gln Ser Pro Val Gln Asp Asn Thr Ser Thr Asn His		
305	310	315
Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asp Arg Lys Leu Tyr		320
325	330	335
Ala Asp Phe Ser His Asp Asn Ser Met Ile Ser Ile Phe Phe Ala Met		
340	345	350
Gly Leu Tyr Asn Gly Thr Gln Pro Leu Ser Met Asp Ser Val Glu Ser		
355	360	365
Ile Gln Glu Met Asp Gly Tyr Ala Ala Ser Trp Thr Val Pro Phe Gly		
370	375	380
Ala Arg Ala Tyr Phe Glu Leu Met Gln Cys Glu Lys Lys Glu Pro Leu		
385	390	395
Val Arg Val Leu Val Asn Asp Arg Val Val Pro Leu His Gly Cys Ala		400
405	410	415
Val Asp Lys Phe Gly Arg Cys Thr Leu Asp Asp Trp Val Glu Gly Leu		
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<212> DNA
<213> Talaromyces thermophilus

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Met Ser Leu

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ttg ttg ctg gtg ctg tcc ggc ggg ttg gtc gcg tta tag tatgctcctt 345

Leu Leu Leu Val Leu Ser Gly Gly Leu Val Ala Leu

5

10

15

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Val Ser Arg Asn

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ccg cat gtt gat agc cac tct tgc aat aca gtg gaa gga ggg tat cag 450

Pro His Val Asp Ser His Ser Cys Asn Thr Val Glu Gly Gly Tyr Gln

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30

35

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Cys Arg Pro Glu Ile Ser His Ser Trp Gly Gln Tyr Ser Pro Phe Phe

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tcc ctg gca gac cag tgc gag atc tgc cca gat gtc cca cag aac tgc 546

Ser Leu Ala Asp Gln Ser Glu Ile Ser Pro Asp Val Pro Gln Asn Cys

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65

aag att acg ttt gtc cag ctg ctt tct cgt cac ggc gct aga tac cct 594

Lys Ile Thr Phe Val Gln Leu Leu Ser Arg His Gly Ala Arg Tyr Pro

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75

80

acg tct tcc aag acg gag ctg tat tgc cag ctg atc agt cgg att cag	642
Thr Ser Ser Lys Thr Glu Leu Tyr Ser Gln Leu Ile Ser Arg Ile Gln	
85 90 95 100	
aag acg gcg act gcg tac aaa ggc tac tat gcc ttc ttg aaa gac tac	690
Lys Thr Ala Thr Ala Tyr Lys Gly Tyr Tyr Ala Phe Leu Lys Asp Tyr	
105 110 115	
aga tac cag ctg gga gcg aac gac ctg acg ccc ttt ggg gaa aac cag	738
Arg Tyr Gln Leu Gly Ala Asn Asp Leu Thr Pro Phe Gly Glu Asn Gln	
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Met Ile Gln Leu Gly Ile Lys Phe Tyr Asn His Tyr Lys Ser Leu Ala	
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Arg Asn Ala Val Pro Phe Val Arg Cys Ser Gly Ser Asp Arg Val Ile	
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gcc tcg ggg aga ctt ttc atc gaa ggt ttc cag agc gcc aaa gtg ctg	882
Ala Ser Gly Arg Leu Phe Ile Glu Gly Phe Gln Ser Ala Lys Val Leu	
165 170 175 180	
gat cct cat tca gac aag cat gac gct cct ccc acg atc aac gtg atc	930
Asp Pro His Ser Asp Lys His Asp Ala Pro Pro Thr Ile Asn Val Ile	
185 190 195	
atc gag gag ggt ccg tcc tac aat aac acg ctc gac acc ggc agc tgt	978
Ile Glu Glu Gly Pro Ser Tyr Asn Asn Thr Leu Asp Thr Gly Ser Cys	
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cca gtc ttt gag gac agc agc ggg gga cat gac gca cag gaa aag ttc	1026
Pro Val Phe Glu Asp Ser Ser Gly Gly His Asp Ala Gln Glu Lys Phe	
215 220 225	
gca aag caa ttc gca cca gct atc ctg gaa aag atc aag gac cat ctt	1074
Ala Lys Gln Phe Ala Pro Ala Ile Leu Glu Lys Ile Lys Asp His Leu	
230 235 240	
ccc ggc gtg gac ctg gcc gtg tgc gat gta ccg tac ttg atg gac ttg	1122
Pro Gly Val Asp Leu Ala Val Ser Asp Val Pro Tyr Leu Met Asp Leu	
245 250 255 260	
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Cys Pro Phe Glu Thr Leu Ala Arg Asn His Thr Asp Thr Leu Ser Pro	
265 270 275	

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Phe Cys Ala Leu Ser Thr Gln Glu Glu Trp Gln Ala Tyr Asp Tyr Tyr	
280 285 290	
caa agt ctg ggg aaa tac tat ggc aat ggc ggg ggt aac ccg ttg ggg	1266
Gln Ser Leu Gly Lys Tyr Tyr Gly Asn Gly Gly Gly Asn Pro Leu Gly	
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Pro Ala Gln Gly Val Gly Phe Val Asn Glu Leu Ile Ala Arg Met Thr	
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His Ser Pro Val Gln Asp Tyr Thr Thr Val Asn His Thr Leu Asp Ser	
325 330 335 340	
aat ccg gcg aca ttc cct ttg aac gcg acg ctg tac gca gat ttc agc	1410
Asn Pro Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser	
345 350 355	
cac gac aac aca atg acg tca att ttc gcg gcc ttg ggc ctg tac aac	1458
His Asp Asn Thr Met Thr Ser Ile Phe Ala Ala Leu Gly Leu Tyr Asn	
360 365 370	
ggg acc gcg aag ctg tcc acg acc gag atc aag tcc att gaa gag acg	1506
Gly Thr Ala Lys Leu Ser Thr Thr Glu Ile Lys Ser Ile Glu Glu Thr	
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Asp Gly Tyr Ser Ala Ala Trp Thr Val Pro Phe Gly Gly Arg Ala Tyr	
390 395 400	
atc gag atg atg cag tgt gat gat tcg gat gag cca gtc gtt cgg gtg	1602
Ile Glu Met Met Gln Cys Asp Asp Ser Asp Glu Pro Val Val Arg Val	
405 410 415 420	
ctg gtc aac gac cgg gtg gtg cca ctg cat ggc tgc gag gtg gac tcc	1650
Leu Val Asn Asp Arg Val Val Pro Leu His Gly Cys Glu Val Asp Ser	
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Leu Gly Arg Cys Lys Arg Asp Asp Phe Val Arg Gly Leu Ser Phe Ala	
440 445 450	
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Arg Gln Gly Gly Asn Trp Glu Gly Cys Tyr Ala Ala Ser Glu	
455 460 465	

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 Val Ser Arg Asn Pro His Val Asp Ser His Ser Cys Asn Thr Val Glu
 1 5 10 15
 Gly Gly Tyr Gln Cys Arg Pro Glu Ile Ser His Ser Trp Gly Gln Tyr
 20 25 30
 Ser Pro Phe Phe Ser Leu Ala Asp Gln Ser Glu Ile Ser Pro Asp Val
 35 40 45
 Pro Gln Asn Cys Lys Ile Thr Phe Val Gln Leu Leu Ser Arg His Gly
 50 55 60
 Ala Arg Tyr Pro Thr Ser Ser Lys Thr Glu Leu Tyr Ser Gln Leu Ile
 65 70 75 80
 Ser Arg Ile Gln Lys Thr Ala Thr Ala Tyr Lys Gly Tyr Tyr Ala Phe
 85 90 95
 Leu Lys Asp Tyr Arg Tyr Gln Leu Gly Ala Asn Asp Leu Thr Pro Phe
 100 105 110
 Gly Glu Asn Gln Met Ile Gln Leu Gly Ile Lys Phe Tyr Asn His Tyr
 115 120 125
 Lys Ser Leu Ala Arg Asn Ala Val Pro Phe Val Arg Cys Ser Gly Ser
 130 135 140
 Asp Arg Val Ile Ala Ser Gly Arg Leu Phe Ile Glu Gly Phe Gln Ser
 145 150 155 160
 Ala Lys Val Leu Asp Pro His Ser Asp Lys His Asp Ala Pro Pro Thr
 165 170 175
 Ile Asn Val Ile Ile Glu Glu Gly Pro Ser Tyr Asn Asn Thr Leu Asp
 180 185 190
 Thr Gly Ser Cys Pro Val Phe Glu Asp Ser Ser Gly Gly His Asp Ala
 195 200 205
 Gln Glu Lys Phe Ala Lys Gln Phe Ala Pro Ala Ile Leu Glu Lys Ile

207020" 3482900T

210	215	220
Lys Asp His Leu Pro Gly Val Asp Leu Ala Val Ser Asp Val Pro Tyr		
225	230	235
Leu Met Asp Leu Cys Pro Phe Glu Thr Leu Ala Arg Asn His Thr Asp		240
	245	250
Thr Leu Ser Pro Phe Cys Ala Leu Ser Thr Gln Glu Glu Trp Gln Ala		255
	260	265
Tyr Asp Tyr Tyr Gln Ser Leu Gly Lys Tyr Tyr Gly Asn Gly Gly Gly		270
	275	280
Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Val Asn Glu Leu Ile		285
	290	295
Ala Arg Met Thr His Ser Pro Val Gln Asp Tyr Thr Thr Val Asn His		300
305	310	315
Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr		320
	325	330
Ala Asp Phe Ser His Asp Asn Thr Met Thr Ser Ile Phe Ala Ala Leu		335
	340	345
Gly Leu Tyr Asn Gly Thr Ala Lys Leu Ser Thr Thr Glu Ile Lys Ser		350
	355	360
Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ala Trp Thr Val Pro Phe Gly		365
	370	375
Gly Arg Ala Tyr Ile Glu Met Met Gln Cys Asp Asp Ser Asp Glu Pro		380
385	390	395
Val Val Arg Val Leu Val Asn Asp Arg Val Val Pro Leu His Gly Cys		400
	405	410
Glu Val Asp Ser Leu Gly Arg Cys Lys Arg Asp Asp Phe Val Arg Gly		415
	420	425
Leu Ser Phe Ala Arg Gln Gly Gly Asn Trp Glu Gly Cys Tyr Ala Ala		430
	435	440
Ser Glu		445
450		

<210> 10
 <211> 1571
 <212> DNA
 <213> Aspergillus fumigatus

<220>
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 <222> (43)..(90)

<220>
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Thr Phe Leu Leu Ser Ala Ala Tyr Leu Leu Ser Gly
5 10 15

ggatctattg ctccgatagg gctgtggtgc tgattctgaa acggagt aga gtg tct 156
Arg Val Ser

gcg gca cct agt tct gct ggc tcc aag tcc tgc gat acg gta gac ctc 204
Ala Ala Pro Ser Ser Ala Gly Ser Lys Ser Cys Asp Thr Val Asp Leu
20 25 30 35

ggg tac cag tgc tcc cct gcg act tct cat cta tgg ggc cag tac tcg 252
Gly Tyr Gln Cys Ser Pro Ala Thr Ser His Leu Trp Gly Gln Tyr Ser
40 45 50

cca ttc ttt tcg ctc gag gac gag ctg tcc gtg tcg agt aag ctt ccc 300
Pro Phe Phe Ser Leu Glu Asp Glu Leu Ser Val Ser Ser Lys Leu Pro
55 60 65

aag gat tgc cgg atc acc ttg gta cag gtg cta tcg cgc cat gga gcg 348
Lys Asp Cys Arg Ile Thr Leu Val Gln Val Leu Ser Arg His Gly Ala
70 75 80

cgg tac cca acc agc tcc aag agc aaa aag tat aag aag ctt gtg acg 396
Arg Tyr Pro Thr Ser Ser Lys Ser Lys Lys Tyr Lys Lys Leu Val Thr
85 90 95

gcg atc cag gcc aat gcc acc gac ttc aag ggc aag ttt gcc ttt ttg 444
Ala Ile Gln Ala Asn Ala Thr Asp Phe Lys Gly Lys Phe Ala Phe Leu
100 105 110 115

aag acg tac aac tat act ctg ggt gcg gat gac ctc act ccc ttt ggg 492
Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly
120 125 130

gag cag cag ctg gtg aac tcg ggc atc aag ttc tac cag agg tac aag 540
Glu Gln Gln Leu Val Asn Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Lys
135 140 145

gct ctg gcg cgc agt gtg gtg ccg ttt att cgc gcc tca ggc tcg gac 588
Ala Leu Ala Arg Ser Val Val Pro Phe Ile Arg Ala Ser Gly Ser Asp
150 155 160

cgg gtt att gct tcg gga gag aag ttc atc gag ggg ttc cag cag gcg 636

Arg Val Ile Ala Ser Gly Glu Lys Phe Ile Glu Gly Phe Gln Gln Ala	
165	170 175
aag ctg gct gat cct ggc gcg acg aac cgc gcc gct ccg gcg att agt	684
Lys Leu Ala Asp Pro Gly Ala Thr Asn Arg Ala Ala Pro Ala Ile Ser	
180	185 190 195
gtg att att ccg gag agc gag acg ttc aac aat acg ctg gac cac ggt	732
Val Ile Ile Pro Glu Ser Glu Thr Phe Asn Asn Thr Leu Asp His Gly	
	200 205 210
gtg tgc acg aag ttt gag gcg agt cag ctg gga gat gag gtt gcg gcc	780
Val Cys Thr Lys Phe Glu Ala Ser Gln Leu Gly Asp Glu Val Ala Ala	
	215 220 225
aat ttc act gcg ctc ttt gca ccc gac atc cga gct cgc gcc gag aag	828
Asn Phe Thr Ala Leu Phe Ala Pro Asp Ile Arg Ala Arg Ala Glu Lys	
	230 235 240
cat ctt cct ggc gtg acg ctg aca gac gag gac gtt gtc agt cta atg	876
His Leu Pro Gly Val Thr Leu Thr Asp Glu Asp Val Val Ser Leu Met	
	245 250 255
gac atg tgt tcg ttt gat acg gta gcg cgc acc agc gac gca agt cag	924
Asp Met Cys Ser Phe Asp Thr Val Ala Arg Thr Ser Asp Ala Ser Gln	
	260 265 270 275
ctg tca ccg ttc tgt caa ctc ttc act cac aat gag tgg aag aag tac	972
Leu Ser Pro Phe Cys Gln Leu Phe Thr His Asn Glu Trp Lys Lys Tyr	
	280 285 290
aac tac ctt cag tcc ttg ggc aag tac tac ggc tac ggc gca ggc aac	1020
Asn Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly Tyr Gly Ala Gly Asn	
	295 300 305
cct ctg gga ccg gct cag ggg ata ggg ttc acc aac gag ctg att gcc	1068
Pro Leu Gly Pro Ala Gln Gly Ile Gly Phe Thr Asn Glu Leu Ile Ala	
	310 315 320
cgg ttg act cgt tcg cca gtg cag gac cac acc agc act aac tcg act	1116
Arg Leu Thr Arg Ser Pro Val Gln Asp His Thr Ser Thr Asn Ser Thr	
	325 330 335
cta gtc tcc aac ccg gcc acc ttc ccg ttg aac gct acc atg tac gtc	1164
Leu Val Ser Asn Pro Ala Thr Phe Pro Leu Asn Ala Thr Met Tyr Val	
	340 345 350 355
gac ttt tca cac gac aac agc atg gtt tcc atc ttc ttt gca ttg ggc	1212

Asp Phe Ser His Asp Asn Ser Met Val Ser Ile Phe Phe Ala Leu Gly
 360 365 370

ctg tac aac ggc act gaa ccc ttg tcc cgg acc tcg gtg gaa agc gcc 1260
 Leu Tyr Asn Gly Thr Glu Pro Leu Ser Arg Thr Ser Val Glu Ser Ala
 375 380 385

aag gaa ttg gat ggg tat tct gca tcc tgg gtg gtg cct ttc ggc gcg 1308
 Lys Glu Leu Asp Gly Tyr Ser Ala Ser Trp Val Val Pro Phe Gly Ala
 390 395 400

cga gcc tac ttc gag acg atg caa tgc aag tcg gaa aag gag cct ctt 1356
 Arg Ala Tyr Phe Glu Thr Met Gln Cys Lys Ser Glu Lys Glu Pro Leu
 405 410 415

gtt cgc gct ttg att aat gac cgg gtt gtg cca ctg cat ggc tgc gat 1404
 Val Arg Ala Leu Ile Asn Asp Arg Val Val Pro Leu His Gly Cys Asp
 420 425 430 435

gtg gac aag ctg ggg cga tgc aag ctg aat gac ttt gtc aag gga ttg 1452
 Val Asp Lys Leu Gly Arg Cys Lys Leu Asn Asp Phe Val Lys Gly Leu
 440 445 450

agt tgg gcc aga tct ggg ggc aac tgg gga gag tgc ttt agt 1494
 Ser Trp Ala Arg Ser Gly Gly Asn Trp Gly Glu Cys Phe Ser
 455 460 465

tgagatgtca ttgttatgct atactccaat agaccgttgc ttagccattc acttcacttt 1554

gctcgaaccg cctgccg 1571

<210> 11

<211> 16

<212> PRT

<213> Aspergillus fumigatus

<400> 11

Met Val Thr Leu Thr Phe Leu Leu Ser Ala Ala Tyr Leu Leu Ser Gly
 1 5 10 15

<210> 12

<211> 449

<212> PRT

<213> Aspergillus fumigatus

<400> 12

10062843.020102

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Val	Asp	Leu	Gly	Tyr	Gln	Cys	Ser	Pro	Ala	Thr	Ser	His	Leu	Trp	Gly	20	25	30	
Gln	Tyr	Ser	Pro	Phe	Phe	Ser	Leu	Glu	Asp	Glu	Leu	Ser	Val	Ser	Ser	35	40	45	
Lys	Leu	Pro	Lys	Asp	Cys	Arg	Ile	Thr	Leu	Val	Gln	Val	Leu	Ser	Arg	50	55	60	
His	Gly	Ala	Arg	Tyr	Pro	Thr	Ser	Ser	Lys	Ser	Lys	Lys	Tyr	Lys	Lys	65	70	75	80
Leu	Val	Thr	Ala	Ile	Gln	Ala	Asn	Ala	Thr	Asp	Phe	Lys	Gly	Lys	Phe	85	90	95	
Ala	Phe	Leu	Lys	Thr	Tyr	Asn	Tyr	Thr	Leu	Gly	Ala	Asp	Asp	Leu	Thr	100	105	110	
Pro	Phe	Gly	Glu	Gln	Gln	Leu	Val	Asn	Ser	Gly	Ile	Lys	Phe	Tyr	Gln	115	120	125	
Arg	Tyr	Lys	Ala	Leu	Ala	Arg	Ser	Val	Val	Pro	Phe	Ile	Arg	Ala	Ser	130	135	140	
Gly	Ser	Asp	Arg	Val	Ile	Ala	Ser	Gly	Glu	Lys	Phe	Ile	Glu	Gly	Phe	145	150	155	160
Gln	Gln	Ala	Lys	Leu	Ala	Asp	Pro	Gly	Ala	Thr	Asn	Arg	Ala	Ala	Pro	165	170	175	
Ala	Ile	Ser	Val	Ile	Ile	Pro	Glu	Ser	Glu	Thr	Phe	Asn	Asn	Thr	Leu	180	185	190	
Asp	His	Gly	Val	Cys	Thr	Lys	Phe	Glu	Ala	Ser	Gln	Leu	Gly	Asp	Glu	195	200	205	
Val	Ala	Ala	Asn	Phe	Thr	Ala	Leu	Phe	Ala	Pro	Asp	Ile	Arg	Ala	Arg	210	215	220	
Ala	Glu	Lys	His	Leu	Pro	Gly	Val	Thr	Leu	Thr	Asp	Glu	Asp	Val	Val	225	230	235	240
Ser	Leu	Met	Asp	Met	Cys	Ser	Phe	Asp	Thr	Val	Ala	Arg	Thr	Ser	Asp	245	250	255	
Ala	Ser	Gln	Leu	Ser	Pro	Phe	Cys	Gln	Leu	Phe	Thr	His	Asn	Glu	Trp	260	265	270	
Lys	Lys	Tyr	Asn	Tyr	Leu	Gln	Ser	Leu	Gly	Lys	Tyr	Tyr	Gly	Tyr	Gly	275	280	285	
Ala	Gly	Asn	Pro	Leu	Gly	Pro	Ala	Gln	Gly	Ile	Gly	Phe	Thr	Asn	Glu	290	295	300	
Leu	Ile	Ala	Arg	Leu	Thr	Arg	Ser	Pro	Val	Gln	Asp	His	Thr	Ser	Thr	305	310	315	320
Asn	Ser	Thr	Leu	Val	Ser	Asn	Pro	Ala	Thr	Phe	Pro	Leu	Asn	Ala	Thr	325	330	335	
Met	Tyr	Val	Asp	Phe	Ser	His	Asp	Asn	Ser	Met	Val	Ser	Ile	Phe	Phe	340	345	350	
Ala	Leu	Gly	Leu	Tyr	Asn	Gly	Thr	Glu	Pro	Leu	Ser	Arg	Thr	Ser	Val	355	360	365	
Glu	Ser	Ala	Lys	Glu	Leu	Asp	Gly	Tyr	Ser	Ala	Ser	Trp	Val	Val	Pro	370	375	380	

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<220>
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Met Gly Val Phe Val Val Leu Leu Ser Ile Ala
1 5 10

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aaacagtaca gc aca tcg ggc act gcg ctg ggc ccc cgt gga aat cac agc 216
          Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn His Ser
                20                25

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cat aaa tgg ggt ctc tac gcg ccc tat ttc tcc ctc cag gat gaa tct 312
His Lys Trp Gly Leu Tyr Ala Pro Tyr Phe Ser Leu Gln Asp Glu Ser
50 55 60

10062848 "020102"

ccg ttt cct ctg gac gtc ccg gat gac tgc cac atc acc ttt gtg cag	360
Pro Phe Pro Leu Asp Val Pro Asp Asp Cys His Ile Thr Phe Val Gln	
65 70 75	
gtg ctg gcc cga cat gga gcg cgg tct cca acc gat agc aag aca aag	408
Val Leu Ala Arg His Gly Ala Arg Ser Pro Thr Asp Ser Lys Thr Lys	
80 85 90	
gcg tat gcc gcg act att gca gcc atc cag aag aat gcc acc gcg ttg	456
Ala Tyr Ala Ala Thr Ile Ala Ala Ile Gln Lys Asn Ala Thr Ala Leu	
95 100 105	
ccg ggc aaa tac gcc ttc ctg aag tcg tac aat tac tcc atg ggc tcc	504
Pro Gly Lys Tyr Ala Phe Leu Lys Ser Tyr Asn Tyr Ser Met Gly Ser	
110 115 120 125	
gag aac ctg aac ccc ttc ggg cgg aac caa ctg caa gat ctg ggc gcc	552
Glu Asn Leu Asn Pro Phe Gly Arg Asn Gln Leu Gln Asp Leu Gly Ala	
130 135 140	
cag ttc tac cgt cgc tac gac acc ctc acc cgg cac atc aac cct ttc	600
Gln Phe Tyr Arg Arg Tyr Asp Thr Leu Thr Arg His Ile Asn Pro Phe	
145 150 155	
gtc cgg gcc gcg gat tcc tcc cgc gtc cac gaa tca gcc gag aag ttc	648
Val Arg Ala Ala Asp Ser Ser Arg Val His Glu Ser Ala Glu Lys Phe	
160 165 170	
gtc gag ggc ttc caa aac gcc cgc caa ggc gat cct cac gcc aac cct	696
Val Glu Gly Phe Gln Asn Ala Arg Gln Gly Asp Pro His Ala Asn Pro	
175 180 185	
cac cag ccg tcg ccg cgc gtg gat gta gtc atc ccc gaa ggc acc gcc	744
His Gln Pro Ser Pro Arg Val Asp Val Val Ile Pro Glu Gly Thr Ala	
190 195 200 205	
tac aac aac acg ctc gag cac agc atc tgc acc gcc ttc gag gcc agc	792
Tyr Asn Asn Thr Leu Glu His Ser Ile Cys Thr Ala Phe Glu Ala Ser	
210 215 220	
acc gtc ggc gac gcc gcg gca gac aac ttc act gcc gtg ttc gcg ccg	840
Thr Val Gly Asp Ala Ala Ala Asp Asn Phe Thr Ala Val Phe Ala Pro	
225 230 235	
gcg atc gcc aag cgt ctg gag gcc gat ctg ccc ggc gtg cag ctg tcc	888
Ala Ile Ala Lys Arg Leu Glu Ala Asp Leu Pro Gly Val Gln Leu Ser	
240 245 250	

gcc gac gac gtg gtc aat ctg atg gcc atg tgt ccg ttc gag acg gtc Ala Asp Asp Val Val Asn Leu Met Ala Met Cys Pro Phe Glu Thr Val 255 260 265	936
agc ctg acc gac gac gcg cac acg ctg tcg ccg ttc tgc gac ctc ttc Ser Leu Thr Asp Asp Ala His Thr Leu Ser Pro Phe Cys Asp Leu Phe 270 275 280 285	984
acc gcc gcc gag tgg acg cag tac aac tac ctg ctc tcg ctg gac aag Thr Ala Ala Glu Trp Thr Gln Tyr Asn Tyr Leu Leu Ser Leu Asp Lys 290 295 300	1032
tac tac ggc tac ggc ggc ggc aat ccg ctg ggc ccc gtg cag ggc gtg Tyr Tyr Gly Tyr Gly Gly Gly Asn Pro Leu Gly Pro Val Gln Gly Val 305 310 315	1080
ggc tgg gcg aac gag ctg atc gcg cgg ctg acg cgc tcc ccc gtc cac Gly Trp Ala Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val His 320 325 330	1128
gac cac acc tgc gtc aac aac acc ctc gac gcc aac ccg gcc acc ttc Asp His Thr Cys Val Asn Asn Thr Leu Asp Ala Asn Pro Ala Thr Phe 335 340 345	1176
ccg ctg aac gcc acc ctc tac gcg gac ttt tcg cac gac agt aac ctg Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Ser Asn Leu 350 355 360 365	1224
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tcg cag acc acc gtg gag gat atc acc cgg acg gac ggg tac gcg gcc Ser Gln Thr Thr Val Glu Asp Ile Thr Arg Thr Asp Gly Tyr Ala Ala 385 390 395	1320
gcc tgg acg gtg ccg ttt gcc gcc cgc gcc tac atc gag atg atg cag Ala Trp Thr Val Pro Phe Ala Ala Arg Ala Tyr Ile Glu Met Met Gln 400 405 410	1368
tgt cgc gcg gag aag cag ccg ctg gtg cgc gtg ctg gtc aac gac cgt Cys Arg Ala Glu Lys Gln Pro Leu Val Arg Val Leu Val Asn Asp Arg 415 420 425	1416
gtc atg ccg ctg cac ggc tgc gcg gtg gat aat ctg ggc agg tgt aaa Val Met Pro Leu His Gly Cys Ala Val Asp Asn Leu Gly Arg Cys Lys 430 435 440 445	1464

cgg gac gac ttt gtg gag gga ctg agc ttt gcg cgg gca gga ggg aac 1512
 Arg Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ala Gly Gly Asn
 450 455 460

tgg gcc gag tgt ttc tgatgtacat gctgtagtta gctttgagtc ctgaggtacc 1567
 Trp Ala Glu Cys Phe
 465

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 <212> PRT
 <213> Aspergillus terreus

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 <211> 450
 <212> PRT
 <213> Aspergillus terreus

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 Gly Leu Tyr Ala Pro Tyr Phe Ser Leu Gln Asp Glu Ser Pro Phe Pro
 35 40 45
 Leu Asp Val Pro Asp Asp Cys His Ile Thr Phe Val Gln Val Leu Ala
 50 55 60
 Arg His Gly Ala Arg Ser Pro Thr Asp Ser Lys Thr Lys Ala Tyr Ala
 65 70 75 80
 Ala Thr Ile Ala Ala Ile Gln Lys Asn Ala Thr Ala Leu Pro Gly Lys
 85 90 95
 Tyr Ala Phe Leu Lys Ser Tyr Asn Tyr Ser Met Gly Ser Glu Asn Leu
 100 105 110
 Asn Pro Phe Gly Arg Asn Gln Leu Gln Asp Leu Gly Ala Gln Phe Tyr
 115 120 125
 Arg Arg Tyr Asp Thr Leu Thr Arg His Ile Asn Pro Phe Val Arg Ala
 130 135 140
 Ala Asp Ser Ser Arg Val His Glu Ser Ala Glu Lys Phe Val Glu Gly
 145 150 155 160
 Phe Gln Asn Ala Arg Gln Gly Asp Pro His Ala Asn Pro His Gln Pro
 165 170 175
 Ser Pro Arg Val Asp Val Val Ile Pro Glu Gly Thr Ala Tyr Asn Asn

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180	185	190
Thr Leu Glu His Ser Ile Cys Thr	Ala Phe Glu Ala Ser Thr	Val Gly
195	200	205
Asp Ala Ala Ala Asp Asn Phe Thr	Ala Val Phe Ala Pro Ala	Ile Ala
210	215	220
Lys Arg Leu Glu Ala Asp Leu Pro Gly	Val Gln Leu Ser Ala Asp	Asp
225	230	235
Val Val Asn Leu Met Ala Met Cys Pro	Phe Glu Thr Val Ser Leu	Thr
245	250	255
Asp Asp Ala His Thr Leu Ser Pro Phe	Cys Asp Leu Phe Thr Ala	Ala
260	265	270
Glu Trp Thr Gln Tyr Asn Tyr Leu Leu	Ser Leu Asp Lys Tyr Tyr	Gly
275	280	285
Tyr Gly Gly Gly Asn Pro Leu Gly Pro	Val Gln Gly Val Gly Trp	Ala
290	295	300
Asn Glu Leu Ile Ala Arg Leu Thr Arg	Ser Pro Val His Asp His	Thr
305	310	315
Cys Val Asn Asn Thr Leu Asp Ala Asn	Pro Ala Thr Phe Pro Leu	Asn
325	330	335
Ala Thr Leu Tyr Ala Asp Phe Ser His	Asp Ser Asn Leu Val Ser	Ile
340	345	350
Phe Trp Ala Leu Gly Leu Tyr Asn Gly	Thr Lys Pro Leu Ser Gln	Thr
355	360	365
Thr Val Glu Asp Ile Thr Arg Thr Asp	Gly Tyr Ala Ala Ala Trp	Thr
370	375	380
Val Pro Phe Ala Ala Arg Ala Tyr Ile	Glu Met Met Gln Cys Arg	Ala
385	390	395
Glu Lys Gln Pro Leu Val Arg Val Leu	Val Asn Asp Arg Val Met	Pro
405	410	415
Leu His Gly Cys Ala Val Asp Asn Leu	Gly Arg Cys Lys Arg Asp	Asp
420	425	430
Phe Val Glu Gly Leu Ser Phe Ala Arg	Ala Gly Gly Asn Trp Ala	Glu
435	440	445
Cys Phe		
450		

<210> 16

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nucleotide

Sequence of Primer #39 designed based on

Aspergillus fumigatus ATCC 13073

<400> 16
tatatcatga ttactctgac tttcctgctt tgg

33

<210> 17
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amino Acid
Sequence Corresponding to Primer #39

<400> 17
Met Ile Thr Leu Thr Phe Leu Leu Ser
1 5

<210> 18
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nucleotide
Sequence of Primer #40 designed based on
Aspergillus fumigatus ATCC 13073

<400> 18
tatatagata tctcaactaa agcactctcc

30

<210> 19
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amino Acid
Sequence Corresponding to Primer #40

<400> 19
Gly Glu Cys Phe Ser
1 5

<210> 20
<211> 31

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fum28 PCR
Primer

<400> 20
atatatcggc cgagtgtctg cggcacctag t

31

<210> 21
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fum11 PCR
Primer

<400> 21
tgaggtcatc cgcacccaga g

21

<210> 22
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fum26 PCR
Primer

<400> 22
ctagaattca tgggtgactct gactttcctg ctttcggcgg cgtatctgct ttcc

54

<210> 23
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fum27 PCR
Primer

<400> 23
ggccggaaag cagatacgcc gccgaaagca ggaaagtcag agtcaccatg aatt

54

<210> 24
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer Q27L s

<400> 24
catctatggg gcctgtactc gccattc

27

<210> 25
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer Q27L as

<400> 25
gaatggcgag tacaggcccc atagatg

27

<210> 26
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Amino Acid
Sequence Encoded by Primer Set A

<400> 26
His Leu Trp Gly Leu Tyr Ser Pro Phe
1 5

<210> 27
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer Q274L s

<400> 27

tacaactacc ttctgtcctt gggcaag

27

<210> 28

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer Q274L as

<400> 28

cttgcccaag gacagaaggt agttgta

27

<210> 29

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Amino Acid
Sequence Encoded by Primer Set B

<400> 29

Tyr Asn Tyr Leu Leu Ser Leu Gly Lys

1

5

<210> 30

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer G277D s

<400> 30

cttcagtcct tggacaagta ctacggc

27

<210> 31

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer G277D as

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gccgtagtac ttgtccaagg actgaag

27

<210> 32

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Amino Acid
Sequence encoded by Primer set C

<400> 32

Leu Gln Ser Leu Asp Lys Tyr Tyr Gly

1

5

<210> 33

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer G277D* s

<400> 33

cttctgtcct tggacaagta ctacggc

27

<210> 34

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer G277D*
as

<400> 34

gccgtagtac ttgtccaagg acagaag

27

<210> 35

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Amino Acid
Sequence Encoded by Primer Set D

<400> 35

Leu Leu Ser Leu Asp Lys Tyr Tyr Gly
1 5

<210> 36

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer N340S s

<400> 36

ttttcacacg acagcagcat ggtttcc

27

<210> 37

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer N340S as

<400> 37

ggaaaccatg ctgctgtcgt gtgaaaa

27

<210> 38

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Amino Acid
Sequence Encoded by Primer Set E

<400> 38

Phe Ser His Asp Ser Ser Met Val Ile
1 5

<210> 39
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer G277K s

<400> 39
ccttcagtc ttgaagaagt actacggcta c

31

<210> 40
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer G277K as

<400> 40
gtagccgtag tacttcttca aggactgaag g

31

<210> 41
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Amino Acid
Sequence Encoded by Primer Set F

<400> 41
Leu Gln Ser Leu Lys Lys Tyr Tyr Gly Tyr
1 5 10

<210> 42
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer A205E s

<400> 42

ggagatgagg ttgaggccaa ttctactg

28

<210> 43

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer A205E as

<400> 43

cagtgaatt ggcctcaacc tcctctcc

28

<210> 44

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Amino Acid
Sequence Encoded by Primer Set G

<400> 44

Gly Asp Glu Val Glu Ala Asn Phe Thr

1

5

<210> 45

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer Y282H s

<400> 45

aagtactacg gccacggcgc aggcaac

27

<210> 46

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer Y282H as

<400> 46
gttgccctgcg ccgtggccgt agtactt

27

<210> 47
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Amino Acid
Sequence Encoded by Primer Set H

<400> 47
Lys Tyr Tyr Gly His Gly Ala Gly Asn
1 5

<210> 48
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer AvrII s

<400> 48
gatacggtag acctagggtta ccagtgc

27

<210> 49
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer AvrII as

<400> 49
gcactgggtac cctagggtcta ccgtatc

27

<210> 50
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Amino Acid
Sequence Encoded by Primer Set I

<400> 50

Asp Thr Val Asp Leu Gly Tyr Gln Cys
1 5

<210> 51

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer S66D s

<400> 51

cggtacccaa ccgattcgaa gagcaaaaag

30

<210> 52

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer S66D as

<400> 52

ctttttgctc ttccaatcgg ttgggtaccg

30

<210> 53

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Amino Acid
Sequence Encoded by Primer Set J

<400> 53

Arg Tyr Pro Thr Asp Ser Lys Ser Lys Lys
1 5 10

<210> 54

<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer
S140Y/D141G s

<400> 54
gcgcctcagg ctacggccgg gttattgc

28

<210> 55
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer
S140Y/D141G as

<400> 55
gcaataaccc ggccgtagcc tgaggcgc

28

<210> 56
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Amino Acid
Sequence Encoded by Primer Set K

<400> 56
Ala Ser Gly Tyr Gly Arg Val Ile Ala
1 5

<210> 57
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer S130N s

<400> 57

ctggcgcgca atgtggtgcc gtttattc

28

<210> 58

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer S130N as

<400> 58

gaataaacgg caccacattg cgcgccag

28

<210> 59

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Amino Acid
Sequence Encoded by Primer Set L

<400> 59

Leu Ala Arg Asn Val Val Pro Phe Ile

1

5

<210> 60

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer
R129L/S130N s

<400> 60

gctctggcgc tcaatgtggt gccgtttatt c

31

<210> 61

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer
R129L/S130N as

<400> 61

gaataaacgg caccacattg agcgccagag c

31

<210> 62

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Amino Acid
Sequence Encoded by Primer Set M

<400> 62

Ala Leu Ala Leu Asn Val Val Pro Phe Ile
1 5 10

<210> 63

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer
K167G/R168Q s

<400> 63

gaccatggct ccggacaagc tacgccag

28

<210> 64

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer
K167G/R168Q as

<400> 64

ctggcgtagc ttgtccggag ccatggtc

28

<210> 65

<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Amino Acid
Sequence Encoded by Primer Set N

<400> 65
Asp His Gly Ser Gly Gln Ala Thr Pro
1 5

<210> 66
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:FumG27-s from
Primer Set O

<400> 66
ctagggtacc agtgctcccc tgcgacttct catctatggg gcggatactc gccattcttt 60
tcgc 64

<210> 67
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:FumG27-as from
Primer Set O

<400> 67
tcgagcgaaa agaatggcga gtatccgccc catagatgag aagtcgcagg ggagcactgg 60
tacc 64

<210> 68
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:FumV27-s from

Primer Set P

<400> 68

ctagggtacc agtgcctccc tgcgacttct catctatggg gcgtgtactc gccattcttt 60
tcgc 64

<210> 69

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:FumV27-as from
Primer Set P

<400> 69

tcgagcgaaa agaatggcga gtacacgccc catagatgag aagtcgcagg ggagcactgg 60
tacc 64

<210> 70

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:FumN27-s from
Primer Set Q

<400> 70

ctagggtacc agtgcctccc tgcgacttct catctatggg gcaactactc gccattcttt 60
tcgc 64

<210> 71

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:FumN27-as from
Primer Set Q

<400> 71

tcgagcgaaa agaatggcga gtagttgccc catagatgag aagtcgcagg ggagcactgg 60
tacc 64

<210> 72
 <211> 64
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:FumI27-s from
 Primer Set R

<400> 72
 ctaggggtacc agtgctcccc tgcgacttct catctatggg gcactctactc gccattcttt 60
 tcgc 64

<210> 73
 <211> 64
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:FumI27-as from
 Primer Set R

<400> 73
 tcgagcgaaa agaattggcga gtagatgccc catagatgag aagtcgcagg ggagcactgg 60
 tacc 64

<210> 74
 <211> 64
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:FumA27-s from
 Primer Set S

<400> 74
 ctaggggtacc agtgctcccc tgcgacttct catctatggg gcgcgtactc gccattcttt 60
 tcgc 64

<210> 75
 <211> 64
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:FumA27-as from
Primer Set S

<400> 75

tcgagcgaaa agaatggcga gtacgcgcc catagatgag aagtcgcagg ggagcactgg 60
tacc 64

<210> 76

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:FumT27-s from
Primer Set T

<400> 76

ctaggggtacc agtgctcccc tgcgacttct catctatggg gcacgtactc gccattcttt 60
tcgc 64

<210> 77

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:FumT27-as from
Primer Set T

<400> 77

tcgagcgaaa agaatggcga gtacgtgcc catagatgag aagtcgcagg ggagcactgg 60
tacc 64

<210> 78

<211> 465

<212> PRT

<213> Aspergillus fumigatus

<400> 78

Met Val Thr Leu Thr Phe Leu Leu Ser Ala Ala Tyr Leu Leu Ser Gly
1 5 10 15

Arg Val Ser Ala Ala Pro Ser Ser Ala Gly Ser Lys Ser Cys Asp Thr
20 25 30

Val Asp Leu Gly Tyr Gln Cys Ser Pro Ala Thr Ser His Leu Trp Gly
35 40 45

Gln Tyr Ser Pro Phe Phe Ser Leu Glu Asp Glu Leu Ser Val Ser Ser
50 55 60

Lys Leu Pro Lys Asp Cys Arg Ile Thr Leu Val Gln Val Leu Ser Arg
65 70 75 80

His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Lys Tyr Lys Lys
85 90 95

Leu Val Thr Ala Ile Gln Ala Asn Ala Thr Asp Phe Lys Gly Lys Phe
100 105 110

Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu Thr
115 120 125

Pro Phe Gly Glu Gln Gln Leu Val Asn Ser Gly Ile Lys Phe Tyr Gln
130 135 140

Arg Tyr Lys Ala Leu Ala Arg Ser Val Val Pro Phe Ile Arg Ala Ser
145 150 155 160

Gly Ser Asp Arg Val Ile Ala Ser Gly Glu Lys Phe Ile Glu Gly Phe
165 170 175

Gln Gln Ala Lys Leu Ala Asp Pro Gly Ala Thr Asn Arg Ala Ala Pro
180 185 190

Ala Ile Ser Val Ile Ile Pro Glu Ser Glu Thr Phe Asn Asn Thr Leu
195 200 205

Asp His Gly Val Cys Thr Lys Phe Glu Ala Ser Gln Leu Gly Asp Glu
210 215 220

Val Ala Ala Asn Phe Thr Ala Leu Phe Ala Pro Asp Ile Arg Ala Arg
225 230 235 240

Ala Glu Lys His Leu Pro Gly Val Thr Leu Thr Asp Glu Asp Val Val
245 250 255

Ser Leu Met Asp Met Cys Ser Phe Asp Thr Val Ala Arg Thr Ser Asp
260 265 270

Ala Ser Gln Leu Ser Pro Phe Cys Gln Leu Phe Thr His Asn Glu Trp
275 280 285

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Lys Lys Tyr Asn Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly Tyr Gly
290 295 300

Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Ile Gly Phe Thr Asn Glu
305 310 315 320

Leu Ile Ala Arg Leu Thr Arg Ser Pro Val Gln Asp His Thr Ser Thr
325 330 335

Asn Ser Thr Leu Val Ser Asn Pro Ala Thr Phe Pro Leu Asn Ala Thr
340 345 350

Met Tyr Val Asp Phe Ser His Asp Asn Ser Met Val Ser Ile Phe Phe
355 360 365

Ala Leu Gly Leu Tyr Asn Gly Thr Glu Pro Leu Ser Arg Thr Ser Val
370 375 380

Glu Ser Ala Lys Glu Leu Asp Gly Tyr Ser Ala Ser Trp Val Val Pro
385 390 395 400

Phe Gly Ala Arg Ala Tyr Phe Glu Thr Met Gln Cys Lys Ser Glu Lys
405 410 415

Glu Pro Leu Val Arg Ala Leu Ile Asn Asp Arg Val Val Pro Leu His
420 425 430

Gly Cys Asp Val Asp Lys Leu Gly Arg Cys Lys Leu Asn Asp Phe Val
435 440 445

Lys Gly Leu Ser Trp Ala Arg Ser Gly Gly Asn Trp Gly Glu Cys Phe
450 455 460

Ser
465

<210> 79

<211> 465

<212> PRT

<213> Aspergillus fumigatus

<400> 79

Met Val Thr Leu Thr Phe Leu Leu Ser Ala Ala Tyr Leu Leu Ser Gly
1 5 10 15

Arg Val Ser Ala Ala Pro Ser Ser Ala Gly Ser Lys Ser Cys Asp Thr

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20	25	30
Val Asp Leu Gly Tyr Gln Cys Ser Pro Ala Thr Ser His Leu Trp Gly		
35	40	45
Gln Tyr Ser Pro Phe Phe Ser Leu Glu Asp Glu Leu Ser Val Ser Ser		
50	55	60
Lys Leu Pro Lys Asp Cys Arg Ile Thr Leu Val Gln Val Leu Ser Arg		
65	70	75 80
His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Lys Tyr Lys Lys		
85	90	95
Leu Val Thr Ala Ile Gln Ala Asn Ala Thr Asp Phe Lys Gly Lys Phe		
100	105	110
Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu Thr		
115	120	125
Pro Phe Gly Glu Gln Gln Leu Val Asn Ser Gly Ile Lys Phe Tyr Gln		
130	135	140
Arg Tyr Lys Ala Leu Ala Arg Ser Val Val Pro Phe Ile Arg Ala Ser		
145	150	155 160
Gly Ser Asp Arg Val Ile Ala Ser Gly Glu Lys Phe Ile Glu Gly Phe		
165	170	175
Gln Gln Ala Lys Leu Ala Asp Pro Gly Ala Thr Asn Arg Ala Ala Pro		
180	185	190
Ala Ile Ser Val Ile Ile Pro Glu Ser Glu Thr Phe Asn Asn Thr Leu		
195	200	205
Asp His Gly Val Cys Thr Lys Phe Glu Ala Ser Gln Leu Gly Asp Glu		
210	215	220
Val Ala Ala Asn Phe Thr Ala Leu Phe Ala Pro Asp Ile Arg Ala Arg		
225	230	235 240
Ala Glu Lys His Leu Pro Gly Val Thr Leu Thr Asp Glu Asp Val Val		
245	250	255
Ser Leu Met Asp Met Cys Ser Phe Asp Thr Val Ala Arg Thr Ser Asp		
260	265	270
Ala Ser Gln Leu Ser Pro Phe Cys Gln Leu Phe Thr His Asn Glu Trp		

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275	280	285
Lys Lys Tyr Asn Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly Tyr Gly		
290	295	300
Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Ile Gly Phe Thr Asn Glu		
305	310	315 320
Leu Ile Ala Arg Leu Thr Arg Ser Pro Val Gln Asp His Thr Ser Thr		
	325	330 335
Asn Ser Thr Leu Val Ser Asn Pro Ala Thr Phe Pro Leu Asn Ala Thr		
	340	345 350
Met Tyr Val Asp Phe Ser His Asp Asn Ser Met Val Ser Ile Phe Phe		
	355	360 365
Ala Leu Gly Leu Tyr Asn Gly Thr Glu Gly Leu Ser Arg Thr Ser Val		
	370	375 380
Glu Ser Ala Lys Glu Leu Asp Gly Tyr Ser Ala Ser Trp Val Val Pro		
385	390	395 400
Phe Gly Ala Arg Ala Tyr Phe Glu Thr Met Gln Cys Lys Ser Glu Lys		
	405	410 415
Glu Pro Leu Val Arg Ala Leu Ile Asn Asp Arg Val Val Pro Leu His		
	420	425 430
Gly Cys Asp Val Asp Lys Leu Gly Arg Cys Lys Leu Asn Asp Phe Val		
	435	440 445
Lys Gly Leu Ser Trp Ala Arg Ser Gly Gly Asn Trp Gly Glu Cys Phe		
	450	455 460
Ser		
465		
<210> 80		
<211> 465		
<212> PRT		
<213> Aspergillus fumigatus		
<400> 80		
Met Val Thr Leu Thr Phe Leu Leu Ser Ala Ala Tyr Leu Leu Ser Gly		
1	5	10 15

Arg Val Ser Ala Ala Pro Ser Ser Ala Gly Ser Lys Ser Cys Asp Thr
20 25 30

Val Asp Leu Gly Tyr Gln Cys Ser Pro Ala Thr Ser His Leu Trp Gly
35 40 45

Gln Tyr Ser Pro Phe Phe Ser Leu Glu Asp Glu Leu Ser Val Ser Ser
50 55 60

Lys Leu Pro Lys Asp Cys Arg Ile Thr Leu Val Gln Val Leu Ser Arg
65 70 75 80

His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Lys Tyr Lys Lys
85 90 95

Leu Val Thr Ala Ile Gln Ala Asn Ala Thr Asp Phe Lys Gly Lys Phe
100 105 110

Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu Thr
115 120 125

Pro Phe Gly Glu Gln Gln Leu Val Asn Ser Gly Ile Lys Phe Tyr Gln
130 135 140

Arg Tyr Lys Ala Leu Ala Arg Ser Val Val Pro Phe Ile Arg Ala Ser
145 150 155 160

Gly Ser Asp Arg Val Ile Ala Ser Gly Glu Lys Phe Ile Glu Gly Phe
165 170 175

Gln Gln Ala Lys Leu Ala Asp Pro Gly Ala Thr Asn Arg Ala Ala Pro
180 185 190

Ala Ile Ser Val Ile Ile Pro Glu Ser Glu Thr Phe Asn Asn Thr Leu
195 200 205

Asp His Gly Val Cys Thr Lys Phe Glu Ala Ser Gln Leu Gly Asp Glu
210 215 220

Val Ala Ala Asn Phe Thr Ala Leu Phe Ala Pro Asp Ile Arg Ala Arg
225 230 235 240

Ala Glu Lys His Leu Pro Gly Val Thr Leu Thr Asp Glu Asp Val Val
245 250 255

Ser Leu Met Asp Met Cys Ser Phe Asp Thr Val Ala Arg Thr Ser Asp
260 265 270

Ala Ser Gln Leu Ser Pro Phe Cys Gln Leu Phe Thr His Asn Glu Trp
 275 280 285

Lys Lys Tyr Asn Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly Tyr Gly
 290 295 300

Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Ile Gly Phe Thr Asn Glu
 305 310 315 320

Leu Ile Ala Arg Leu Thr Arg Ser Pro Val Gln Asp His Thr Ser Thr
 325 330 335

Asn Ser Thr Leu Val Ser Asn Pro Ala Thr Phe Pro Leu Asn Ala Thr
 340 345 350

Met Tyr Val Asp Phe Ser His Asp Asn Ser Met Val Ser Ile Phe Phe
 355 360 365

Ala Leu Gly Leu Tyr Asn Gly Thr Glu Pro Leu Ser Arg Thr Ser Val
 370 375 380

Glu Ser Ala Lys Glu Leu Asp Gly Tyr Ser Ala Ser Trp Val Val Pro
 385 390 395 400

Phe Gly Ala Arg Ala Tyr Phe Glu Thr Met Gln Cys Lys Ser Glu Lys
 405 410 415

Glu Ser Leu Val Arg Ala Leu Ile Asn Asp Arg Val Val Pro Leu His
 420 425 430

Gly Cys Asp Val Asp Lys Leu Gly Arg Cys Lys Leu Asn Asp Phe Val
 435 440 445

Lys Gly Leu Ser Trp Ala Arg Ser Gly Gly Asn Trp Gly Glu Cys Phe
 450 455 460

Ser
 465

<210> 81

<211> 465

<212> PRT

<213> Aspergillus fumigatus

<400> 81

Met Val Thr Leu Thr Phe Leu Leu Ser Ala Ala Tyr Leu Leu Ser Gly
 1 5 10 15

Arg Val Ser Ala Ala Pro Ser Ser Ala Gly Ser Lys Ser Cys Asp Thr
 20 25 30

Val Asp Leu Gly Tyr Gln Cys Ser Pro Ala Thr Ser His Leu Trp Gly
 35 40 45

Gln Tyr Ser Pro Phe Phe Ser Leu Glu Asp Glu Leu Ser Val Ser Ser
 50 55 60

Lys Leu Pro Lys Asp Cys Arg Ile Thr Leu Val Gln Val Leu Ser Arg
 65 70 75 80

His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Lys Tyr Lys Lys
 85 90 95

Leu Val Thr Ala Ile Gln Ala Asn Ala Thr Asp Phe Lys Gly Lys Phe
 100 105 110

Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu Thr
 115 120 125

Ala Phe Gly Glu Gln Gln Leu Val Asn Ser Gly Ile Lys Phe Tyr Gln
 130 135 140

Arg Tyr Lys Ala Leu Ala Arg Ser Val Val Pro Phe Ile Arg Ala Ser
 145 150 155 160

Gly Ser Asp Arg Val Ile Ala Ser Gly Glu Lys Phe Ile Glu Gly Phe
 165 170 175

Gln Gln Ala Lys Leu Ala Asp Pro Gly Ala Thr Asn Arg Ala Ala Pro
 180 185 190

Ala Ile Ser Val Ile Ile Pro Glu Ser Glu Thr Phe Asn Asn Thr Leu
 195 200 205

Asp His Gly Val Cys Thr Lys Phe Glu Ala Ser Gln Leu Gly Asp Glu
 210 215 220

Val Ala Ala Asn Phe Thr Ala Leu Phe Ala Pro Asp Ile Arg Ala Arg
 225 230 235 240

Ala Lys Lys His Leu Pro Gly Val Thr Leu Thr Asp Glu Asp Val Val
 245 250 255

Ser Leu Met Asp Met Cys Ser Phe Asp Thr Val Ala Arg Thr Ser Asp
 260 265 270

Ala Ser Gln Leu Ser Pro Phe Cys Gln Leu Phe Thr His Asn Glu Trp
 275 280 285

Lys Lys Tyr Asn Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly Tyr Gly
 290 295 300

Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Ile Gly Phe Thr Asn Glu
 305 310 315 320

Leu Ile Ala Arg Leu Thr Arg Ser Pro Val Gln Asp His Thr Ser Thr
 325 330 335

Asn Ser Thr Leu Val Ser Asn Pro Ala Thr Phe Pro Leu Asn Ala Thr
 340 345 350

Met Tyr Val Asp Phe Ser His Asp Asn Ser Met Val Ser Ile Phe Phe
 355 360 365

Ala Leu Gly Leu Tyr Asn Gly Thr Glu Pro Leu Ser Arg Thr Ser Val
 370 375 380

Glu Ser Ala Lys Glu Leu Asp Gly Tyr Ser Ala Ser Trp Val Val Pro
 385 390 395 400

Phe Gly Ala Arg Ala Tyr Phe Glu Thr Met Gln Cys Lys Ser Glu Lys
 405 410 415

Glu Pro Leu Val Arg Ala Leu Ile Asn Asp Arg Val Val Pro Leu His
 420 425 430

Gly Cys Asp Val Asp Lys Leu Gly Arg Cys Lys Leu Asn Asp Phe Val
 435 440 445

Lys Gly Leu Ser Trp Ala Arg Ser Gly Gly Asn Trp Gly Glu Cys Phe
 450 455 460

Ser
 465

<210> 82

<211> 469

<212> PRT

<213> Aspergillus fumigatus

<400> 82

Met Gly Ala Leu Thr Phe Leu Leu Ser Val Met Tyr Leu Leu Ser Gly

1 5 10 15
 Val Ala Gly Ala Pro Ser Ser Gly Cys Ser Ala Gly Ser Gly Ser Lys
 20 25 30
 Ala Cys Asp Thr Val Glu Leu Gly Tyr Gln Cys Ser Pro Gly Thr Ser
 35 40 45
 His Leu Trp Gly Gln Tyr Ser Pro Phe Phe Ser Leu Glu Asp Glu Leu
 50 55 60
 Ser Val Ser Ser Asp Leu Pro Lys Asp Cys Arg Val Thr Phe Val Gln
 65 70 75 80
 Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Ala Ser Lys Ser Lys
 85 90 95
 Lys Tyr Lys Lys Leu Val Thr Ala Ile Gln Lys Asn Ala Thr Glu Phe
 100 105 110
 Lys Gly Lys Phe Ala Phe Leu Glu Thr Tyr Asn Tyr Thr Leu Gly Ala
 115 120 125
 Asp Asp Leu Thr Pro Phe Gly Glu Gln Gln Met Val Asn Ser Gly Ile
 130 135 140
 Lys Phe Tyr Gln Lys Tyr Lys Ala Leu Ala Gly Ser Val Val Pro Phe
 145 150 155 160
 Ile Arg Ser Ser Gly Ser Asp Arg Val Ile Ala Ser Gly Glu Lys Phe
 165 170 175
 Ile Glu Gly Phe Gln Gln Ala Asn Val Ala Asp Pro Gly Ala Thr Asn
 180 185 190
 Arg Ala Ala Pro Val Ile Ser Val Ile Ile Pro Glu Ser Glu Thr Tyr
 195 200 205
 Asn Asn Thr Leu Asp His Ser Val Cys Thr Asn Phe Glu Ala Ser Glu
 210 215 220
 Leu Gly Asp Glu Val Glu Ala Asn Phe Thr Ala Leu Phe Ala Pro Ala
 225 230 235 240
 Ile Arg Ala Arg Ile Glu Lys His Leu Pro Gly Val Gln Leu Thr Asp
 245 250 255
 Asp Asp Val Val Ser Leu Met Asp Met Cys Ser Phe Asp Thr Val Ala

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260	265	270
Arg Thr Ala Asp Ala Ser Glu Leu Ser Pro Phe Cys Ala Ile Phe Thr		
275	280	285
His Asn Glu Trp Lys Lys Tyr Asp Tyr Leu Gln Ser Leu Gly Lys Tyr		
290	295	300
Tyr Gly Tyr Gly Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Ile Gly		
305	310	315 320
Phe Thr Asn Glu Leu Ile Ala Arg Leu Thr Asn Ser Pro Val Gln Asp		
325	330	335
His Thr Ser Thr Asn Ser Thr Leu Asp Ser Asp Pro Ala Thr Phe Pro		
340	345	350
Leu Asn Ala Thr Ile Tyr Val Asp Phe Ser His Asp Asn Gly Met Ile		
355	360	365
Pro Ile Phe Phe Ala Met Gly Leu Tyr Asn Gly Thr Glu Pro Leu Ser		
370	375	380
Gln Thr Ser Glu Glu Ser Thr Lys Glu Ser Asn Gly Tyr Ser Ala Ser		
385	390	395 400
Trp Ala Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu Thr Met Gln Cys		
405	410	415
Lys Ser Glu Lys Glu Pro Leu Val Arg Ala Leu Ile Asn Asp Arg Val		
420	425	430
Val Pro Leu His Gly Cys Ala Val Asp Lys Leu Gly Arg Cys Lys Leu		
435	440	445
Lys Asp Phe Val Lys Gly Leu Ser Trp Ala Arg Ser Gly Gly Asn Ser		
450	455	460
Glu Gln Ser Phe Ser		
465		